

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/591,099
Source: IFWP
Date Processed by STIC: 9/12/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 09/12/2006

PATENT APPLICATION: US/10/591,099

TIME: 11:06:57

Input Set : A:\082368-010000US.txt

Output Set: N:\CRF4\09122006\J591099.raw

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4 <110> APPLICANT: Matsui, Takeshi
5     Kisumi, Fumie
6     Kinoshita, Yoko
8 <120> TITLE OF INVENTION: NOVEL GENE PARTICIPATING IN EPIDERMAL
9     DIFFERENTIATION AND USE THEREOF
11 <130> FILE REFERENCE: 082368-010000US
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/591,099
C--> 13 <141> CURRENT FILING DATE: 2006-08-29
13 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/03458
14 <151> PRIOR FILING DATE: 2005-03-02
16 <150> PRIOR APPLICATION NUMBER: JP 2004-057559
17 <151> PRIOR FILING DATE: 2004-03-02
19 <160> NUMBER OF SEQ ID NOS: 53
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 661
25 <212> TYPE: DNA
26 <213> ORGANISM: Mus musculus
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (23)..(337)
31 <223> OTHER INFORMATION:
W--> 33 <400> 1
34 ctgactgtac gagagcacaa cc atg aaa cca gtc acg gcc tct gct ctg ctg      52
35                               Met Lys Pro Val Thr Ala Ser Ala Leu Leu
36                               1           5           10
38 ctt atc ctg ctg ggt gtg gcc tgg cgt gga gac agc cac agc tgg ggt      100
39 Leu Ile Leu Leu Gly Val Ala Trp Arg Gly Asp Ser His Ser Trp Gly
40                               15           20           25
42 tca gat ctg tca tct ctg cag aag agg gca ggt gga gct gac cag ttt      148
43 Ser Asp Leu Ser Ser Leu Gln Lys Arg Ala Gly Gly Ala Asp Gln Phe
44                               30           35           40
46 tct aag cct gaa gca aga caa gat ctt tca gct gac tca tcc aag aac      196
47 Ser Lys Pro Glu Ala Arg Gln Asp Leu Ser Ala Asp Ser Ser Lys Asn
48                               45           50           55
50 tac tac aat aac cag cag gtg aat cct act tac aac tgg caa tac tat      244
51 Tyr Tyr Asn Asn Gln Gln Val Asn Pro Thr Tyr Asn Trp Gln Tyr Tyr
52                               60           65           70
54 acc aag acc act gcc aag gcg gga gtc aca cct tca tct tcc tcg gct      292
55 Thr Lys Thr Thr Ala Lys Ala Gly Val Thr Pro Ser Ser Ser Ser Ala
56 75                               80           85           90
58 tcc cgg gca caa cct ggc ctg ctg aag tgg ctg aag ttt tgg tag      337
59 Ser Arg Ala Gln Pro Gly Leu Leu Lys Trp Leu Lys Phe Trp

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60          95          100
62 aacattcctt ctagtcaactg cggactcctc acgaatgcac acaggtcttc agggagtttg 397
64 actgtcctta cccagagtcc tctctgatgc agctgaccta cctgggcatg acaagcctgt 457
66 catctcgctt ggggacctgg tttatctgtc ctcattctcc ccattcgatt gtgggtgtctt 517
68 ggcgactaat cagtttcatt gtataaccag ccagatcttc acctcttctt ccgtacgtga 577
70 ccgcaagtcc ctggaacgag gcatctggag cttcctactc tccagtttct ctgtggaaat 637
72 aaaacatgac tctttgtttc cctg 661

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75 <210> SEQ ID NO: 2

76 <211> LENGTH: 104

77 <212> TYPE: PRT

78 <213> ORGANISM: Mus musculus

80 <400> SEQUENCE: 2

81 Met Lys Pro Val Thr Ala Ser Ala Leu Leu Leu Ile Leu Leu Gly Val

82 1 5 10 15

84 Ala Trp Arg Gly Asp Ser His Ser Trp Gly Ser Asp Leu Ser Ser Leu

85 20 25 30

87 Gln Lys Arg Ala Gly Gly Ala Asp Gln Phe Ser Lys Pro Glu Ala Arg

88 35 40 45

90 Gln Asp Leu Ser Ala Asp Ser Ser Lys Asn Tyr Tyr Asn Asn Gln Gln

91 50 55 60

93 Val Asn Pro Thr Tyr Asn Trp Gln Tyr Tyr Thr Lys Thr Thr Ala Lys

94 65 70 75 80

96 Ala Gly Val Thr Pro Ser Ser Ser Ala Ser Arg Ala Gln Pro Gly

97 85 90 95

99 Leu Leu Lys Trp Leu Lys Phe Trp

100 100

103 <210> SEQ ID NO: 3

104 <211> LENGTH: 2043

105 <212> TYPE: DNA

106 <213> ORGANISM: Mus musculus

108 <220> FEATURE:

109 <221> NAME/KEY: CDS

110 <222> LOCATION: (170)..(1723)

111 <223> OTHER INFORMATION:

W--> 113 <400> 3

114 gctggaaagc agggaagtct gggaacagag agagaaggct gtgggtcctg gggaaggaga 60

116 ataaggaagc aaggaaggaa aggaaaaggc ctcagcccag aggaagaaag aagggaacaa 120

118 atagactggg ctgcagacat cctcagagga gagaggggagc tgggcagag atg aag cta 178

119 Met Lys Leu

120 1

122 cag ggc tct ctg gcc tgc ctc ctg ctg gcc cta tgt ctg ggt ggt ggg 226

123 Gln Gly Ser Leu Ala Cys Leu Leu Leu Ala Leu Cys Leu Gly Gly Gly

124 5 10 15

126 gca gct aac ccg ctg cac agt gga ggg gag ggc aca ggg gca agt gct 274

127 Ala Ala Asn Pro Leu His Ser Gly Gly Glu Gly Thr Gly Ala Ser Ala

128 20 25 30 35

130 gcc cat gga gca gga gat gcc att agc cat gga att gga gag gct gtg 322

131 Ala His Gly Ala Gly Asp Ala Ile Ser His Gly Ile Gly Glu Ala Val

132 40 45 50

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134	ggc	caa	ggg	gct	aaa	gaa	gca	gcc	agc	tct	gga	atc	cag	aat	gcc	cta	370
135	Gly	Gln	Gly	Ala	Lys	Glu	Ala	Ala	Ser	Ser	Gly	Ile	Gln	Asn	Ala	Leu	
136			55						60					65			
138	ggc	cag	ggg	cac	gga	gag	gaa	ggg	ggc	tcc	aca	ttg	atg	ggg	agc	aga	418
139	Gly	Gln	Gly	His	Gly	Glu	Glu	Gly	Gly	Ser	Thr	Leu	Met	Gly	Ser	Arg	
140			70					75					80				
142	ggc	gat	gtt	ttt	gag	cac	cgg	ctt	ggg	gaa	gca	gca	aga	tct	ctg	ggg	466
143	Gly	Asp	Val	Phe	Glu	His	Arg	Leu	Gly	Glu	Ala	Ala	Arg	Ser	Leu	Gly	
144		85					90					95					
146	aac	gct	ggg	aat	gag	att	ggc	aga	cag	gct	gag	gat	atc	att	cgc	caa	514
147	Asn	Ala	Gly	Asn	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Ile	Ile	Arg	Gln	
148	100					105					110				115		
150	ggg	gta	gat	gct	gtc	cac	aac	gct	ggg	tcc	tgg	ggg	aca	tct	gga	ggg	562
151	Gly	Val	Asp	Ala	Val	His	Asn	Ala	Gly	Ser	Trp	Gly	Thr	Ser	Gly	Gly	
152				120						125					130		
154	cat	ggc	gca	tat	ggc	tct	caa	ggg	ggg	gct	gga	gtc	cag	ggc	aat	cct	610
155	His	Gly	Ala	Tyr	Gly	Ser	Gln	Gly	Gly	Ala	Gly	Val	Gln	Gly	Asn	Pro	
156			135						140					145			
158	ggg	cct	caa	ggg	aca	ccc	tgg	gcc	tca	gga	ggc	aac	tat	ggg	act	aac	658
159	Gly	Pro	Gln	Gly	Thr	Pro	Trp	Ala	Ser	Gly	Gly	Asn	Tyr	Gly	Thr	Asn	
160			150					155					160				
162	tct	ctg	ggg	ggc	tct	gtg	ggg	cag	ggg	ggc	aat	ggc	gga	cca	ctc	aac	706
163	Ser	Leu	Gly	Gly	Ser	Val	Gly	Gln	Gly	Gly	Asn	Gly	Gly	Pro	Leu	Asn	
164		165					170					175					
166	tat	gaa	acc	aat	gcc	cag	gga	gct	gtg	gct	cag	cct	ggc	tac	ggg	aca	754
167	Tyr	Glu	Thr	Asn	Ala	Gln	Gly	Ala	Val	Ala	Gln	Pro	Gly	Tyr	Gly	Thr	
168	180					185					190				195		
170	gtg	aga	ggc	aac	aac	cag	aac	tca	ggg	tgt	acc	aac	ccc	cca	cct	tct	802
171	Val	Arg	Gly	Asn	Asn	Gln	Asn	Ser	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	
172				200						205					210		
174	ggc	tcc	cat	gaa	agc	ttc	agt	aac	tct	ggg	gga	agc	agc	aat	gat	ggc	850
175	Gly	Ser	His	Glu	Ser	Phe	Ser	Asn	Ser	Gly	Gly	Ser	Ser	Asn	Asp	Gly	
176			215						220					225			
178	agt	cgt	ggg	agc	caa	ggc	agt	cat	ggc	agt	aat	ggg	cag	ggc	agc	agc	898
179	Ser	Arg	Gly	Ser	Gln	Gly	Ser	His	Gly	Ser	Asn	Gly	Gln	Gly	Ser	Ser	
180			230					235					240				
182	ggg	aga	ggc	ggg	ggc	caa	ggc	aac	agc	gac	aac	aat	ggc	agc	agt	agc	946
183	Gly	Arg	Gly	Gly	Gly	Gln	Gly	Asn	Ser	Asp	Asn	Asn	Gly	Ser	Ser	Ser	
184		245					250					255					
186	agt	agc	agc	ggc	agc	aac	agt	ggc	aac	agc	aac	agt	ggc	aac	agc	ggc	994
187	Ser	Ser	Ser	Gly	Ser	Asn	Ser	Gly	Asn	Ser	Asn	Ser	Gly	Asn	Ser	Gly	
188	260					265					270				275		
190	aac	agc	aac	agt	ggc	aac	agc	ggc	aac	agc	ggg	tct	ggg	tcc	cgg	gac	1042
191	Asn	Ser	Asn	Ser	Gly	Asn	Ser	Gly	Asn	Ser	Gly	Ser	Gly	Ser	Arg	Asp	
192				280					285						290		
194	ata	gaa	aca	tct	aat	ttt	gat	gaa	ggc	tat	tcg	gtc	tcc	agg	gga	acc	1090
195	Ile	Glu	Thr	Ser	Asn	Phe	Asp	Glu	Gly	Tyr	Ser	Val	Ser	Arg	Gly	Thr	
196				295					300					305			
198	ggc	agc	agg	ggg	gga	agt	ggg	gga	agt	ggg	gga	agt	ggg	gga	agt	ggg	1138

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199 Gly Ser Arg Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
200          310          315          320
202 gga agt ggt gga agt ggt ggt gga aac aaa ccc gag tgt aac aac cca      1186
203 Gly Ser Gly Gly Ser Gly Gly Gly Asn Lys Pro Glu Cys Asn Asn Pro
204          325          330          335
206 ggg aat gat gtg cgc atg gcc gga gga tct ggg agt cag ggg cat ggg      1234
207 Gly Asn Asp Val Arg Met Ala Gly Gly Ser Gly Ser Gln Gly His Gly
208 340          345          350          355
210 tcc aat ggt ggc aat ata caa aaa gaa gct gtc aat gga ctc aac act      1282
211 Ser Asn Gly Gly Asn Ile Gln Lys Glu Ala Val Asn Gly Leu Asn Thr
212          360          365          370
214 atg aac tcg gat gca tct acc ttg ccc ttc aac att gac aat ttc tgg      1330
215 Met Asn Ser Asp Ala Ser Thr Leu Pro Phe Asn Ile Asp Asn Phe Trp
216          375          380          385
218 gag aat ctt aag tcc aag acg cgc ttc att aac tgg gat gcc ata aac      1378
219 Glu Asn Leu Lys Ser Lys Thr Arg Phe Ile Asn Trp Asp Ala Ile Asn
220          390          395          400
222 aag ggt cat gcc cca tct ccc agc act cgg gct tta ctc tac ttc cgc      1426
223 Lys Gly His Ala Pro Ser Pro Ser Thr Arg Ala Leu Leu Tyr Phe Arg
224          405          410          415
226 aaa ctg tgg gag aat ttc aaa cgc agc act cct ttc ttc aac tgg aaa      1474
227 Lys Leu Trp Glu Asn Phe Lys Arg Ser Thr Pro Phe Phe Asn Trp Lys
228 420          425          430          435
230 cag att gag ggt tca gat ctg tca tct ctg cag aag agg gca ggt gga      1522
231 Gln Ile Glu Gly Ser Asp Leu Ser Ser Leu Gln Lys Arg Ala Gly Gly
232          440          445          450
234 gct gac cag ttt tct aag cct gaa gca aga caa gat ctt tca gct gac      1570
235 Ala Asp Gln Phe Ser Lys Pro Glu Ala Arg Gln Asp Leu Ser Ala Asp
236          455          460          465
238 tca tcc aag aac tac tac aat aac cag cag gtg aat cct act tac aac      1618
239 Ser Ser Lys Asn Tyr Tyr Asn Asn Gln Gln Val Asn Pro Thr Tyr Asn
240          470          475          480
242 tgg caa tac tat acc aag acc act gcc aag gcg gga gtc aca cct tca      1666
243 Trp Gln Tyr Tyr Thr Lys Thr Thr Ala Lys Ala Gly Val Thr Pro Ser
244          485          490          495
246 tct tcc tcg gct tcc cgg gca caa cct ggc ctg ctg aag tgg ctg aag      1714
247 Ser Ser Ser Ala Ser Arg Ala Gln Pro Gly Leu Leu Lys Trp Leu Lys
248 500          505          510          515
250 ttt tgg tag aacattcctt ctagtctactg cggactcctc acgaatgcac      1763
251 Phe Trp
254 acaggctcttc agggagtttg actgtcctta cccagagtcc tctctgatgc agctgacctc      1823
256 cctgggcatg acaagcctgt catctcgctt ggggacctgg tttatctgtc ctcattctcc      1883
258 ccattcgatt gtggtgtctt ggcgactaat cagtttcatt gtataaccag ccagatcttc      1943
260 acctcttctt ccgtacgtga ccgcaagtcc ctggaacgag gcactctggag cttcctactc      2003
262 tccagtttct ctgtggaaat aaaacatgac tctttgtttc      2043
265 <210> SEQ ID NO: 4
266 <211> LENGTH: 517
267 <212> TYPE: PRT
268 <213> ORGANISM: Mus musculus

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270 <400> SEQUENCE: 4

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271 Met Lys Leu Gln Gly Ser Leu Ala Cys Leu Leu Leu Ala Leu Cys Leu
272 1 5 10 15
274 Gly Gly Gly Ala Ala Asn Pro Leu His Ser Gly Gly Glu Gly Thr Gly
275 20 25 30
277 Ala Ser Ala Ala His Gly Ala Gly Asp Ala Ile Ser His Gly Ile Gly
278 35 40 45
280 Glu Ala Val Gly Gln Gly Ala Lys Glu Ala Ala Ser Ser Gly Ile Gln
281 50 55 60
283 Asn Ala Leu Gly Gln Gly His Gly Glu Glu Gly Gly Ser Thr Leu Met
284 65 70 75 80
286 Gly Ser Arg Gly Asp Val Phe Glu His Arg Leu Gly Glu Ala Ala Arg
287 85 90 95
289 Ser Leu Gly Asn Ala Gly Asn Glu Ile Gly Arg Gln Ala Glu Asp Ile
290 100 105 110
292 Ile Arg Gln Gly Val Asp Ala Val His Asn Ala Gly Ser Trp Gly Thr
293 115 120 125
295 Ser Gly Gly His Gly Ala Tyr Gly Ser Gln Gly Gly Ala Gly Val Gln
296 130 135 140
298 Gly Asn Pro Gly Pro Gln Gly Thr Pro Trp Ala Ser Gly Gly Asn Tyr
299 145 150 155 160
301 Gly Thr Asn Ser Leu Gly Gly Ser Val Gly Gln Gly Gly Asn Gly Gly
302 165 170 175
304 Pro Leu Asn Tyr Glu Thr Asn Ala Gln Gly Ala Val Ala Gln Pro Gly
305 180 185 190
307 Tyr Gly Thr Val Arg Gly Asn Asn Gln Asn Ser Gly Cys Thr Asn Pro
308 195 200 205
310 Pro Pro Ser Gly Ser His Glu Ser Phe Ser Asn Ser Gly Gly Ser Ser
311 210 215 220
313 Asn Asp Gly Ser Arg Gly Ser Gln Gly Ser His Gly Ser Asn Gly Gln
314 225 230 235 240
316 Gly Ser Ser Gly Arg Gly Gly Gly Gln Gly Asn Ser Asp Asn Asn Gly
317 245 250 255
319 Ser Ser Ser Ser Ser Ser Gly Ser Asn Ser Gly Asn Ser Asn Ser Gly
320 260 265 270
322 Asn Ser Gly Asn Ser Asn Ser Gly Asn Ser Gly Asn Ser Gly Ser Gly
323 275 280 285
325 Ser Arg Asp Ile Glu Thr Ser Asn Phe Asp Glu Gly Tyr Ser Val Ser
326 290 295 300
328 Arg Gly Thr Gly Ser Arg Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
329 305 310 315 320
331 Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Asn Lys Pro Glu Cys
332 325 330 335
334 Asn Asn Pro Gly Asn Asp Val Arg Met Ala Gly Gly Ser Gly Ser Gln
335 340 345 350
337 Gly His Gly Ser Asn Gly Gly Asn Ile Gln Lys Glu Ala Val Asn Gly
338 355 360 365
340 Leu Asn Thr Met Asn Ser Asp Ala Ser Thr Leu Pro Phe Asn Ile Asp
341 370 375 380

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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\082368-010000US.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33

Seq#:34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52

VERIFICATION SUMMARY

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Input Set : A:\082368-010000US.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:31
L:113 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:111
L:381 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:379
L:454 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:452